binding sites being such that relevant regulators or hypothetically introduced regulators are to be bound thereto, the calculation model employing, as parameters, loci of the regulator binding sites or other factors that cause expression of the gene. The level of transcription of the gene with respect to the above-constructed calculation model is computed. Through use of parameter search algorithms, parameters of the calculation model are searched so that empirically known expression of the gene is obtained, to thereby predict microstructures of the enhancer or promoter.

REMARKS

Favorable consideration of this application, as presently amended, is respectfully requested.

The present Preliminary Amendment is submitted to place the above-identified application in more proper format under United States practice.

By the present Preliminary Amendment the multiple dependency in Claim 3 is cancelled and subject matter of the cancelled multiple dependency is set forth in new dependent Claim 6.

The Abstract has also been amended to be in the form of a single paragraph, to no longer recite any reference numerals, and to make minor idiomatic changes thereto.

The present application is believed to be in condition for a full and thorough examination on the merits. An early and favorable consideration of the present application is hereby respectfully requested.

Respectfully submitted,

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IN THE CLAIMS

Please amend the claims as follows:

--3. (Amended) The method for predicting the structure of a gene regulator binding site as described in claim 1 [or 2], wherein, from the searched parameter sets, microstructures comprising binding sites of the enhancer or promoter, some of the binding sites interacting locally with one another, are predicted as follows:

at portions where binding sites are dense, the microstructures are physically close to one another for interaction therebetween, or they are physically remote from one another but interact with one another closely and functionally, and

at portions where binding sites are sparse, the microstructures are physically remote from one another and yet functional, or they are functionally independent from one another.--

Claim 6 (New).

IN THE ABSTRACT

Please amend the Abstract on page 31 as follows:

--ABSTRACT

A method for predicting the structure of a binding site to which a gene regulator binds, which method enables, through investigation of the internal structure of an enhancer or

promoter, transcriptional regulation of a gene can be more clearly elucidated. The method [for predicting the gene regulator binding site structure includes providing] provides a gene of interest, of which a user of the method desires to predict regulation-related structures of binding sites [(12), (13), (14)] to which regulators bind, the binding sites [(12), (13), (14)] being present within an enhancer or promoter [(11)] region to which a protein serving as a transcriptional element is bound and which is present upstream or downstream to a coding region [(15)] of the gene[;]. [constructing a] A calculation model for each of the binding sites [(12), (13), (14)] is constructed within the enhancer or promoter [(11)] region, the binding sites [(12), (13), (14)] being such that relevant regulators or hypothetically introduced regulators are to be bound thereto, the calculation model employing, as parameters, loci of the regulator binding sites or other factors that cause expression of the gene[;]. [computing the] The level of transcription of the gene with respect to the above-constructed calculation model[;] is computed. Through [searching, through] use of parameter search algorithms, parameters of the calculation model are searched so that empirically known expression of the gene is obtained[;], to thereby predict microstructures of the enhancer or promoter.--